

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:49:50 ; Search time 6173 Seconds  
(without alignments)  
11028.605 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 1405

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

8

Result No.	Score	Query			Description	
		Match	Length	DB	ID	
1	958.4	68.2	5925	6	AR268191	AR268191 Sequence
2	958.4	68.2	5925	6	AX009712	AX009712 Sequence

3	958.4	68.2	5925	6	AX010972	AX010972 Sequence
4	937.8	66.7	2186	6	AX744004	AX744004 Sequence
5	937.8	66.7	2790	6	AX744002	AX744002 Sequence
6	937.8	66.7	2810	6	AX744006	AX744006 Sequence
7	936.4	66.6	1440	6	AX744010	AX744010 Sequence
8	901.4	64.2	4691	6	AR370701	AR370701 Sequence
9	901.4	64.2	6166	6	AR370702	AR370702 Sequence
10	779.8	55.5	6563	6	AR116667	AR116667 Sequence
11	779.8	55.5	6563	6	CQ802871	CQ802871 Sequence
12	779.8	55.5	6563	6	AR233026	AR233026 Sequence
13	779.8	55.5	6563	6	AR237957	AR237957 Sequence
14	779.8	55.5	6563	6	BD069220	BD069220 Antibody
15	751.8	53.5	2000	6	AX774567	AX774567 Sequence
16	747.4	53.2	2178	6	AR048108	AR048108 Sequence
17	747.4	53.2	2178	6	AR054190	AR054190 Sequence
18	747.4	53.2	2178	6	BD144975	BD144975 Method fo
19	747.4	53.2	2178	6	BD145002	BD145002 Human gro
20	739.6	52.6	1951	6	AX661181	AX661181 Sequence
21	739.6	52.6	6072	6	AX815239	AX815239 Sequence
22	739.6	52.6	6072	6	BD069267	BD069267 Anti-VEGF
23	738.6	52.6	2143	6	AR123435	AR123435 Sequence
24	738.6	52.6	2143	6	BD132751	BD132751 Antibody
25	738.6	52.6	2143	6	AR261841	AR261841 Sequence
26	738.6	52.6	2143	6	AR491893	AR491893 Sequence
27	738.6	52.6	2143	6	BD062169	BD062169 Protein r
28	738.6	52.6	6550	6	AR126813	AR126813 Sequence
29	738.6	52.6	6550	6	AR162111	AR162111 Sequence
30	738.6	52.6	6550	6	BD224164	BD224164 Method of
31	738.6	52.6	6550	6	AX832563	AX832563 Sequence
32	737.4	52.5	2050	6	CQ861227	CQ861227 Sequence
33	735.2	52.3	6072	6	BD010368	BD010368 Humanized
34	734.6	52.3	6127	6	AR091716	AR091716 Sequence
35	734.6	52.3	6127	6	AR124896	AR124896 Sequence
36	734.6	52.3	6127	6	AR169096	AR169096 Sequence
37	734.6	52.3	6127	6	BD193235	BD193235 Improved
38	734.6	52.3	6127	6	AR454349	AR454349 Sequence
39	734.6	52.3	6127	6	AR527679	AR527679 Sequence
40	689.4	49.1	2239	6	CQ877236	CQ877236 Sequence
41	689.4	49.1	2383	6	CQ877237	CQ877237 Sequence
42	638.2	45.4	784	9	AB064058	AB064058 Homo sapi
43	633.4	45.1	794	9	AB064136	AB064136 Homo sapi
44	632.2	45.0	3169	6	A57359	A57359 Sequence 5
45	632.2	45.0	3169	6	AR096536	AR096536 Sequence

us-10-698-041-1.rng

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:39:44 ; Search time 814 Seconds  
(without alignments)  
10217.735 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 1405

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	1405	100.0	1405	13	ADR16814 Human bre
2	1014.8	72.2	1522	8	Acc00496 Humanised
3	1003	71.4	1514	12	Adg64751 Humanised
4	985.8	70.2	1424	13	Adr16815 Human bre
5	958.4	68.2	5924	3	Aaz38921 hCAT1 bin
6	958.4	68.2	5925	3	Aaz38770 hCAT1 clo
7	937.8	66.7	2186	10	Add26469 Phagmid
8	937.8	66.7	2790	10	Add26467 Phagmid
9	937.8	66.7	2810	10	Add26471 Phagmid
10	936.4	66.6	1440	10	Add26475 Phagmid

us-10-698-041-1.rng

11	923	65.7	1539	8	AAD56202	Aad56202 X5 antibo
12	916.6	65.2	1539	8	AAD56203	Aad56203 X5 antibo
13	906.2	64.5	1680	12	ADF83552	Adf83552 Anti-tete
14	901.4	64.2	4691	2	AAQ92546	Aaq92546 pComb3 ex
15	901.4	64.2	6166	2	AAQ92547	Aaq92547 Expressio
16	884.8	63.0	10251	10	ABZ37478	Abz37478 CJRA05 nu
17	856	60.9	1526	12	ADN97514	Adn97514 Artificia
18	851.8	60.6	1551	12	ADN97496	Adn97496 Artificia
19	834.8	59.4	1566	12	ADN97494	Adn97494 Artificia
20	834	59.4	2154	12	ADN97490	Adn97490 Artificia
21	820.8	58.4	1572	12	ADN97492	Adn97492 Artificia
22	820	58.4	2160	12	ADN97488	Adn97488 Artificia
23	796.8	56.7	5679	13	ADP79576	Adp79576 Plasmid p
24	779.8	55.5	6563	2	AAV44953	Aav44953 Anti-IL-8
25	779.8	55.5	6563	2	AAX90579	Aax90579 p6G4V11N3
26	779.8	55.5	6563	3	AAZ87970	Aaz87970 Nucleotid
27	779.8	55.5	6563	3	AAC65509	Aac65509 Anti-IL-8
28	779.8	55.5	6563	8	ABX63890	Abx63890 Expressio
29	779.8	55.5	6563	8	ABX81417	Abx81417 Vector p6
30	779.8	55.5	6563	10	AAD59311	Aad59311 p6G4V11 N
31	767.8	54.6	6400	3	AAA53389	Aaa53389 Expressio
32	751.8	53.5	2000	9	ACC70052	Acc70052 Nucleotid
33	747.4	53.2	2178	2	AAQ25592	Aaq25592 Encodes 4
34	747.4	53.2	2178	2	AAV81689	Aav81689 4D5 Fab m
35	739.6	52.6	6072	2	AAV63493	Aav63493 Fab-displ
36	739.6	52.6	6072	6	ABN85200	Abn85200 Phage-dis
37	738.6	52.6	2143	2	AAX03840	Aax03840 Plasmid p
38	738.6	52.6	2143	5	AAF31463	Aaf31463 ps 1130 e
39	737.4	52.5	2050	13	ADR47463	Adr47463 pTTOD(gh3
40	735.2	52.3	6072	2	AAV71266	Aav71266 VEGF huma
41	734.6	52.3	6127	2	AAX07474	Aax07474 Mus muscu
42	734.6	52.3	6127	4	AAF69253	Aaf69253 Expressio
43	734.6	52.3	6127	12	ADN07022	Adn07022 F(ab)-pha
44	733.2	52.2	1951	6	ABQ73919	Abq73919 Plasmid p
45	732.8	52.2	1477	12	ADQ07674	Adq07674 Nucleotid

#### ALIGNMENTS

RESULT 1  
ADR16814  
ID ADR16814 standard; DNA; 1405 BP.  
XX  
AC ADR16814;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Human breast cancer-specific antibody Fab fragment DNA, Fab14.6.19.  
XX  
KW Breast cancer; diagnosis; therapy; human; Fab 14.6.19; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 41. .700  
FT /\*tag= a  
FT /product= "Human breast cancer-specific antibody Fab  
FT fragment Fab14.6.19"  
FT /partial  
FT /note= "No start codon"  
FT CDS 797. .1147  
FT /\*tag= b

us-10-698-041-1.rng

/product= "Human breast cancer-specific antibody Fab  
fragment Fab14.6.19"  
/partial  
/note= "No start and stop codon"  
/transl\_except= (pos:1145. .1147, aa:Ser-Xaa)

XX  
PN US2004151724-A1.  
XX  
PD 05-AUG-2004.  
XX  
PF 30-OCT-2003; 2003US-00698041.  
XX  
PR 31-OCT-2002; 2002US-0423052P.  
XX  
PA (CORO/) CORONELLA-WOOD J.  
XX  
PI Coronella-Wood J;  
XX  
DR WPI; 2004-570704/55.  
DR P-PSDB; ADR16816, ADR16817.  
XX  
PT New isolated polynucleotides encoding breast cancer-specific antibody Fab  
PT fragments 14.6.19 and 14.6.20, useful as clinical reagents for diagnosing  
PT or treating breast cancer.  
XX  
PS Claim 1; SEQ ID NO 1; 36pp; English.  
XX  
CC The invention provides a breast cancer-specific antibody fragment  
CC polynucleotide and its corresponding polypeptide. The invention is useful  
CC as clinical reagents for the diagnosis and therapy of breast cancer. The  
CC present sequence is human breast cancer-specific antibody Fab fragment  
CC DNA, Fab14.6.19.  
XX  
SQ Sequence 1405 BP; 326 A; 405 C; 381 G; 293 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 1405; DB 13; Length 1405;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCCAGGCCGGCGAGCTCGTGATGACTCAGTC 60  
Db 1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCCAGGCCGGCGAGCTCGTGATGACTCAGTC 60  
  
Qy 61 TCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCCATCTCCTGCAGGTCTAGTCA 120  
Db 61 TCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCCATCTCCTGCAGGTCTAGTCA 120  
  
Qy 121 GAGTCTCCTGCATAGTAATGGATACAACATTGGATTGGTACCTGCAGAACGCCAGGGCA 180  
Db 121 GAGTCTCCTGCATAGTAATGGATACAACATTGGATTGGTACCTGCAGAACGCCAGGGCA 180  
  
Qy 181 GTCTCCACAGCTCCTGATCTATTGGTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240  
Db 181 GTCTCCACAGCTCCTGATCTATTGGTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240  
  
Qy 241 CAGTGGCAGTGGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300  
Db 241 CAGTGGCAGTGGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300  
  
Qy 301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360  
Db 301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360

## us-10-698-041-1.rng

Qy 361 ACGACTGGAGATTAAACGAACGTGGCTGCACCCTGTCTTCATCTTCCGCCATCTGA 420  
 |||||  
 Db 361 ACGACTGGAGATTAAACGAACGTGGCTGCACCCTGTCTTCATCTTCCGCCATCTGA 420  
 |||||  
 Qy 421 TGAGCAGTTGAAATCTGGAACGTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAG 480  
 |||||  
 Db 421 TGAGCAGTTGAAATCTGGAACGTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAG 480  
 |||||  
 Qy 481 AGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAG 540  
 |||||  
 Db 481 AGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAG 540  
 |||||  
 Qy 541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG 600  
 |||||  
 Db 541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG 600  
 |||||  
 Qy 601 CAAAGCAGACTACGAGAAACACAAAGTACGCCTGCGAAGTCACCCATCAGGGCTGAG 660  
 |||||  
 Db 601 CAAAGCAGACTACGAGAAACACAAAGTACGCCTGCGAAGTCACCCATCAGGGCTGAG 660  
 |||||  
 Qy 661 CTTGCCGTACAAGAGCTTCAACAGGGAGAGTGTAGTTCTAGATAATTAAATTAGGA 720  
 |||||  
 Db 661 CTTGCCGTACAAGAGCTTCAACAGGGAGAGTGTAGTTCTAGATAATTAAATTAGGA 720  
 |||||  
 Qy 721 GGAATTAAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780  
 |||||  
 Db 721 GGAATTAAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780  
 |||||  
 Qy 781 CCAACCAGCCATGGCCAGGTGCAGCTGCAGGAGTCCGGGGAGGCTTAGTTCAGCCTGG 840  
 |||||  
 Db 781 CCAACCAGCCATGGCCAGGTGCAGCTGCAGGAGTCCGGGGAGGCTTAGTTCAGCCTGG 840  
 |||||  
 Qy 841 GGGGTCCCTGAGACTCTCTGTGAAGCCTCTGGATAACACCTCAGCAATTACTGGATGCA 900  
 |||||  
 Db 841 GGGGTCCCTGAGACTCTCTGTGAAGCCTCTGGATAACACCTCAGCAATTACTGGATGCA 900  
 |||||  
 Qy 901 CTGGGTCCGCCAACCTCCAGGGAAAGGGGCTGGTGTGGTCTCACGTATTAATGAAGATGG 960  
 |||||  
 Db 901 CTGGGTCCGCCAACCTCCAGGGAAAGGGGCTGGTGTGGTCTCACGTATTAATGAAGATGG 960  
 |||||  
 Qy 961 GAGTATCACAAACGACGCCGACTCCGTGAAGGGCGATCCACCATCTCCAGAGACAACGC 1020  
 |||||  
 Db 961 GAGTATCACAAACGACGCCGACTCCGTGAAGGGCGATCCACCATCTCCAGAGACAACGC 1020  
 |||||  
 Qy 1021 CAAGAACACGCTGTATCTGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATT 1080  
 |||||  
 Db 1021 CAAGAACACGCTGTATCTGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATT 1080  
 |||||  
 Qy 1081 CTGTACACGAGATATTGGGGTCGTGATGCTCACTGGGCCAGGGAACCCCTGGTACCGT 1140  
 |||||  
 Db 1081 CTGTACACGAGATATTGGGGTCGTGATGCTCACTGGGCCAGGGAACCCCTGGTACCGT 1140  
 |||||  
 Qy 1141 CTCCTAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCCCAAGAGCAC 1200  
 |||||  
 Db 1141 CTCCTAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCCCAAGAGCAC 1200  
 |||||  
 Qy 1201 CTCTGGGGCACAGCGGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC 1260  
 |||||  
 Db 1201 CTCTGGGGCACAGCGGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC 1260  
 |||||  
 Qy 1261 GGTGTCGTGGAACTCAGGCCCTGACCAGGGCGTGACACCTCCGGCTGTCTTACA 1320  
 |||||  
 Db 1261 GGTGTCGTGGAACTCAGGCCCTGACCAGGGCGTGACACCTCCGGCTGTCTTACA 1320

us-10-698-041-1.rng

Qy 1321 GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGCAC 1380  
|||  
Db 1321 GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGCAC 1380  
|||  
Qy 1381 CCAGACCTACATCTGCAACGTGAAT 1405  
|||  
Db 1381 CCAGACCTACATCTGCAACGTGAAT 1405

us-10-698-041-1.rnpb

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 10:58:17 ; Search time 877 Seconds  
(without alignments)  
9719.189 Million cell updates/sec

Title: US-10-698-041-1  
Perfect score: 1405  
Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1405	100.0	1405	18	US-10-698-041-1	Sequence 1, Appli

us-10-698-041-1.rnpb									
2	1003	71.4	1514	17	US-10-251-215-38		Sequence	38,	App1
3	985.8	70.2	1424	18	US-10-698-041-2		Sequence	2,	App1
4	958.4	68.2	5925	16	US-10-235-175-78		Sequence	78,	App1
5	923	65.7	1539	18	US-10-492-729-4		Sequence	4,	App1
6	916.6	65.2	1539	18	US-10-492-729-12		Sequence	12,	App1
7	884.8	63.0	10251	17	US-10-045-674-582		Sequence	582,	App1
8	856	60.9	1526	18	US-10-679-620-87		Sequence	87,	App1
9	851.8	60.6	1551	18	US-10-679-620-69		Sequence	69,	App1
10	834.8	59.4	1566	18	US-10-679-620-67		Sequence	67,	App1
11	834	59.4	2154	18	US-10-679-620-63		Sequence	63,	App1
12	820.8	58.4	1572	18	US-10-679-620-65		Sequence	65,	App1
13	820	58.4	2160	18	US-10-679-620-61		Sequence	61,	App1
14	779.8	55.5	6563	10	US-09-726-258-61		Sequence	61,	App1
15	739.6	52.6	1951	13	US-10-011-125-1		Sequence	1,	App1
16	739.6	52.6	6072	9	US-09-056-160B-99		Sequence	99,	App1
17	739.6	52.6	6072	16	US-10-234-671-99		Sequence	99,	App1
18	738.6	52.6	2143	9	US-09-940-166A-5		Sequence	5,	App1
19	738.6	52.6	2143	18	US-10-762-967-5		Sequence	5,	App1
20	734.6	52.3	6127	9	US-09-920-171-1		Sequence	1,	App1
21	734.6	52.3	6127	15	US-10-113-996-1		Sequence	1,	App1
22	734.6	52.3	6127	18	US-10-791-619-1		Sequence	1,	App1
23	732.8	52.2	1477	19	US-10-728-420B-116		Sequence	116,	App
c	732.8	52.2	1477	19	US-10-728-420B-117		Sequence	117,	App
24	681.6	48.5	1730	14	US-10-194-975-108		Sequence	108,	App
25	628	44.7	720	17	US-10-292-088-15		Sequence	15,	App1
26	627.8	44.7	720	17	US-10-292-088-63		Sequence	63,	App1
27	624.8	44.5	720	17	US-10-292-088-7		Sequence	7,	App1
28	624.8	44.5	720	17	US-10-292-088-101		Sequence	101,	App
29	624.4	44.4	720	17	US-10-292-088-55		Sequence	55,	App1
30	623.2	44.4	720	17	US-10-292-088-79		Sequence	79,	App1
31	621.6	44.2	720	17	US-10-292-088-39		Sequence	39,	App1
32	620	44.1	720	17	US-10-292-088-31		Sequence	31,	App1
33	618.8	44.0	4793	18	US-10-737-290-141		Sequence	141,	App
34	612.6	43.6	1081	17	US-10-466-164-33		Sequence	33,	App1
35	612.2	43.6	657	10	US-09-972-656-103		Sequence	103,	App
36	609.8	43.4	649	19	US-10-714-079C-8		Sequence	8,	App1
37	606.2	43.1	944	17	US-10-108-260A-1585		Sequence	1585,	Ap
38	604.6	43.0	968	10	US-09-992-600A-7		Sequence	7,	App1
39	604.6	43.0	968	10	US-09-924-340-7		Sequence	7,	App1
40	604.6	43.0	968	10	US-09-992-095B-7		Sequence	7,	App1
41	604.6	43.0	968	10	US-09-999-570-7		Sequence	7,	App1
42	604.6	43.0	968	14	US-10-000-489-7		Sequence	7,	App1
43	604.6	43.0	968	14	US-10-000-986-7		Sequence	7,	App1
44	604.6	43.0	968	14	US-10-154-678-7		Sequence	7,	App1
45	604.6	43.0	968	16	US-10-154-678-7		Sequence	7,	App1

## ALIGNMENTS

RESULT 1  
US-10-698-041-1

: Sequence 1, Application US/10698041  
Publication No. US20040151724A1

GENERAL INFORMATION:

APPLICANT: Coronella-Wood, Julia

TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer

FILE REFERENCE: 5051.057

CURRENT APPLICATION NUMBER: US/10/698,041

CURRENT FILING DATE: 2003-10-30

PRIOR APPLICATION NUMBER: US 60/423,052

PRIOR FILING DATE: 2002-10-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.2

## us-10-698-041-1.rnpb

; SEQ ID NO 1  
; LENGTH: 1405  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-698-041-1

Query Match 100.0%; Score 1405; DB 18; Length 1405;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCAGGCAGGCCGAGCTCGTGATGACTCAGTC	60
Db	1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCAGGCAGGCCGAGCTCGTGATGACTCAGTC	60
Qy	61 TCCACTCTCCCTGCCGTACCCCTGGAGAGCCGGCTCCATCTCCTGCAGGTCTAGTCA	120
Db	61 TCCACTCTCCCTGCCGTACCCCTGGAGAGCCGGCTCCATCTCCTGCAGGTCTAGTCA	120
Qy	121 GAGTCTCCTGCATAGTAATGGATACAACATTGGATTGGTACCTGCAGAACGCCAGGGCA	180
Db	121 GAGTCTCCTGCATAGTAATGGATACAACATTGGATTGGTACCTGCAGAACGCCAGGGCA	180
Qy	181 GTCTCACAGCTCCTGATCTATTGGGTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT	240
Db	181 GTCTCACAGCTCCTGATCTATTGGGTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT	240
Qy	241 CAGTGGCAGTGGATCAGGCACAGATTATACTGAAATCAGCAGAGTGGAGGCTGAGGA	300
Db	241 CAGTGGCAGTGGATCAGGCACAGATTATACTGAAATCAGCAGAGTGGAGGCTGAGGA	300
Qy	301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTCGGCCAAGGGAC	360
Db	301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTCGGCCAAGGGAC	360
Qy	361 ACGACTGGAGATTAACGAACGTGGCTGCACCATCTGTTCTATCTCCGCCATCTGA	420
Db	361 ACGACTGGAGATTAACGAACGTGGCTGCACCATCTGTTCTATCTCCGCCATCTGA	420
Qy	421 TGAGCAGTTGAAATCTGAACTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAG	480
Db	421 TGAGCAGTTGAAATCTGAACTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAG	480
Qy	481 AGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGTAACTCCCAGGAGAG	540
Db	481 AGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGTAACTCCCAGGAGAG	540
Qy	541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACGCCCTCAGCAGCACCTGACGCTGAG	600
Db	541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACGCCCTCAGCAGCACCTGACGCTGAG	600
Qy	601 CAAAGCAGACTACGAGAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAG	660
Db	601 CAAAGCAGACTACGAGAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAG	660
Qy	661 CTTGCCGTACAAAGAGCTTCAACAGGGAGAGTGTAGTTCTAGATAATTAGGA	720
Db	661 CTTGCCGTACAAAGAGCTTCAACAGGGAGAGTGTAGTTCTAGATAATTAGGA	720
Qy	721 GGAATTAAAATGAAATACCTATTGCCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC	780
Db	721 GGAATTAAAATGAAATACCTATTGCCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC	780
Qy	781 CCAACCAGCCATGGCCAGGTGCAGCTGCAGGAGTCCGGGGAGGCTAGTTCAGCCTGG	840

us-10-698-041-1.rnpb

Db 781 CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGAGGCTTAGTTCAGCCTGG 840  
Qy 841 GGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATAACACCTTCAGCAATTACTGGATGCA 900  
Db 841 GGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATAACACCTTCAGCAATTACTGGATGCA 900  
Qy 901 CTGGTCCGCCAACCTCCAGGGAAAGGGCTGGTGGGTCTCACGTATTAATGAAGATGG 960  
Db 901 CTGGTCCGCCAACCTCCAGGGAAAGGGCTGGTGGGTCTCACGTATTAATGAAGATGG 960  
Qy 961 GAGTATCACAAACGACCGGACTCCGTGAAGGGCCATCCACCATCTCCAGAGACAACGC 1020  
Db 961 GAGTATCACAAACGACCGGACTCCGTGAAGGGCCATCCACCATCTCCAGAGACAACGC 1020  
Qy 1021 CAAGAACACGCTGTATCTGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATT 1080  
Db 1021 CAAGAACACGCTGTATCTGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATT 1080  
Qy 1081 CTGTACACGAGATATTGGGGTCGTGATGCTCACTGGGCCAGGGAACCCCTGGTACCGT 1140  
Db 1081 CTGTACACGAGATATTGGGGTCGTGATGCTCACTGGGCCAGGGAACCCCTGGTACCGT 1140  
Qy 1141 CTCTCAGCCTCCACCAAGGGCCATCGGTCTCCCCCTGGCACCCCTCCTCCAAGAGCAC 1200  
Db 1141 CTCTCAGCCTCCACCAAGGGCCATCGGTCTCCCCCTGGCACCCCTCCTCCAAGAGCAC 1200  
Qy 1201 CTCTGGGGCACAGCGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC 1260  
Db 1201 CTCTGGGGCACAGCGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC 1260  
Qy 1261 GGTGTCGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACA 1320  
Db 1261 GGTGTCGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACA 1320  
Qy 1321 GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGCAC 1380  
Db 1321 GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGCAC 1380  
Qy 1381 CCAGACCTACATCTGCAACGTGAAT 1405  
Db 1381 CCAGACCTACATCTGCAACGTGAAT 1405

RESULT 2

US-10-251-215-38

; Sequence 38, Application US/10251215

; Publication No. US20030219839A1

GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Kretz-Rommel, Anke

; APPLICANT: Frederickson, Shana

; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 1087-36

; CURRENT APPLICATION NUMBER: US/10/251,215

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: US 60/323,537

; PRIOR FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: US 60/323,544

; PRIOR FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: US 60/379,980

; PRIOR FILING DATE: 2002-05-13

us-10-698-041-1.rnpb

NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 38  
LENGTH: 1514  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Assembled Degenerate Oligonucleotides  
US-10-251-215-38

Query Match 71.4%; Score 1003; DB 17; Length 1514;  
Best Local Similarity 83.7%; Pred. No. 7e-281;  
Matches 1163; Conservative 25; Mismatches 165; Indels 36; Gaps 4;

Qy	35	GCGGCCGAGCTCGTGTGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCCG	94
Db	15	GGGCCGAGATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGA	74
Qy	95	GCCTCCATCTCCTGCAGGCTAGTCAGAGTCTCCTGCATAGTAATGGATAACAATTG	154
Db	75	GTCACCACACTTGCCRGGCSAGTCAGRG CATTAGT-----ARYTACTTA	119
Qy	155	GATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGTTAAAT	214
Db	120	GCCTGGTATCAGCAGAAACCAGGGAAASYTCCTAACGCTCCTGATCTATGATGCATCCGAT	179
Qy	215	CGGGCCTCCGGGTCCCTGACAGGTTAGTGGCAGTGGATCAGGCACAGATTATACTG	274
Db	180	CTGGCATCTGGGTCCCATCTCGGTTARTGGCAGTGGATCTGGACAGATTWCACCTCTC	239
Qy	275	AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCAAG-----	326
Db	240	ACCATCAGCAGCCTGCAGYSTGAAGATGTYGCAACTTATTACTGTCAACAGGGTTAGT	299
Qy	327	-GTCTACAAACTCCTAGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACGTG	385
Db	300	AGTAGTAATGTTGATAATACTTCGGCGAGGGACCGAGGTGGTGTCAAACGAACGTG	359
Qy	386	GCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCC	445
Db	360	GCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCC	419
Qy	446	TCTGTTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTG	505
Db	420	TCTGTTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTG	479
Qy	506	GATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC	565
Db	480	GATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC	539
Qy	566	AGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAA	625
Db	540	AGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAA	599
Qy	626	GTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTGCCGTACAAAGAGCTTCAAC	685
Db	600	GTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTGCCGTACAAAGAGCTTCAAC	659
Qy	686	AGGGGAGAGTGTAGTTCTAGATAATTAGGAGGAATTAAAATGAAATACCTATTG	745
Db	660	AGGGGAGAGTGTAGTTCTAGATAATTAGGAGGAATTAAAATGAAATACCTATTG	719
Qy	746	CCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCAACAGCCATGGCCAGGTGCAG	805

## us-10-698-041-1.rnpb

Db	720	CCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCAACCAACCAGCCATGGCGAGGTGCAG	779
Qy	806	CTGCAGGAGTCGGGGGAGGCTTAGTTAGTCAGCCTGGGGGTCCCTGAGACTCTCCTGTGAA	865
Db	780	CTGGTGGAGTCTGGGGAGGCCTGGTCAAGCCTGGGGGTCCCTGAGACTCTCCTGTGCA	839
Qy	866	GCCTCTGGATACACCTTCAGCAATTACTGGATGCACTGGGTCGCCAACCTCCAGGGAAG	925
Db	840	GCCTCTGGATTWCYYCAGTARMWATRKMATRARYTGGTCCGCCAGGCTCCAGGGAAG	899
Qy	926	GGGCTGGTGTGGTCTCACGTATTAATGAAGATGGGAGTATCACAAACGACGCCGGACTCC	985
Db	900	GGGCTGGAGTGGRTCKSATTCTTAAT---ACTGGTAGTAGCGCATACTACGCGAGCTGG	956
Qy	986	GTGAAGGGCCGATCCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGAAATG	1045
Db	957	GCGGAAAGCCGATYCACCATCTCCAGAGACAMGCCAAGAACACTCASTGTATCTGCAAATG	1016
Qy	1046	AACAGTCTGAGAGCCGAGGACACGGCTGTCTATTACTGTACACGAGATATTGGGGTCGT	1105
Db	1017	AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTWCTGTGCGAGAGGTAGTCCTGGTTAC	1076
Qy	1106	GATGCT-----CACTGGGCCAGGGAACCCCTGGTACCGTCTCCCTAGCCTCCACC	1156
Db	1077	AGTGATGGACTTAACATCTGGGCCAGGGCACCCCTGGTACCGTCTCCCTAGCCTCCACC	1136
Qy	1157	AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCAAAGAGCACCTCTGGGGCACAGCG	1216
Db	1137	AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCAAAGAGCACCTCTGGGGCACAGCG	1196
Qy	1217	GCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTTGAACTCA	1276
Db	1197	GCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTTGAACTCA	1256
Qy	1277	GGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCCTCAGGACTCTAC	1336
Db	1257	GGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCCTCAGGACTCTAC	1316
Qy	1337	TCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGCACCCAGACCTACATCTGC	1396
Db	1317	TCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGCACCCAGACCTACATCTGC	1376
Qy	1397	AACGTGAAT 1405	
Db	1377	AACGTGAAT 1385	

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 07:45:31 ; Search time 4941 Seconds  
(without alignments)  
10823.780 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 1405

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_htc:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
<hr/>						
1	615.4	43.8	995	5	BQ712430	BQ712430 AGENCOURT
2	608	43.3	859	4	BG758795	BG758795 602713155
3	603.8	43.0	785	6	CB958366	CB958366 AGENCOURT
4	600.4	42.7	796	6	CB956719	CB956719 AGENCOURT
5	597.8	42.5	734	6	CB957433	CB957433 AGENCOURT
6	596.6	42.5	908	4	BG685179	BG685179 602637065
7	589.2	41.9	731	6	CB985070	CB985070 AGENCOURT
8	588.4	41.9	730	4	BI837183	BI837183 603089959

9	587.4	41.8	958	5	BQ709417	BQ709417 AGENCOURT	
10	585.8	41.7	880	4	BG755003	BG755003 602711509	
11	582.2	41.4	771	6	CB956254	CB956254 AGENCOURT	
12	576.2	41.0	753	4	BG756401	BG756401 602715727	
13	574.8	40.9	765	6	CB957191	CB957191 AGENCOURT	
14	574	40.9	952	4	BG758592	BG758592 602712820	
15	572	40.7	734	6	CB986286	CB986286 AGENCOURT	
16	569.8	40.6	912	4	BF974515	BF974515 602243421	
17	569.4	40.5	880	4	BG757588	BG757588 602714763	
18	565.4	40.2	766	6	CB956983	CB956983 AGENCOURT	
19	564.2	40.2	710	4	BI908471	BI908471 603069231	
20	563.8	40.1	774	4	BM007808	BM007808 603617276	
21	562.2	40.0	875	4	BI518518	BI518518 603061638	
22	560.2	39.9	898	5	BQ708918	BQ708918 AGENCOURT	
23	558.2	39.7	816	4	BI759427	BI759427 603043095	
24	556	39.6	931	4	BG757255	BG757255 602715238	
25	556	39.6	962	4	BI819546	BI819546 603036758	
26	552.6	39.3	934	4	BF974268	BF974268 602243920	
27	552.4	39.3	817	6	CB957285	CB957285 AGENCOURT	
28	550	39.1	770	4	BG530186	BG530186 602558684	
29	548.8	39.1	839	6	CB986712	CB986712 AGENCOURT	
30	547.4	39.0	751	6	CB956880	CB956880 AGENCOURT	
31	543.8	38.7	811	4	BI818338	BI818338 603032958	
32	543	38.6	743	6	CB987308	CB987308 AGENCOURT	
33	542.2	38.6	824	4	BI824708	BI824708 603033871	
34	539.2	38.4	918	4	BG681688	BG681688 602627806	
c	35	537.2	38.2	615	2	AW603541	AW603541 RC0-CN002
	36	536.4	38.2	795	6	CB958667	CB958667 AGENCOURT
	37	535.8	38.1	849	7	CO578998	CO578998 ILLUMIGEN
	38	533	37.9	706	6	CB956177	CB956177 AGENCOURT
	39	533	37.9	740	6	CB958744	CB958744 AGENCOURT
	40	532.4	37.9	726	4	BM007723	BM007723 603617168
	41	532.4	37.9	731	6	CB955606	CB955606 AGENCOURT
	42	531.4	37.8	697	6	CD684481	CD684481 EST1001 h
	43	531	37.8	971	7	CO580847	CO580847 ILLUMIGEN
	44	530	37.7	907	5	BQ708655	BQ708655 AGENCOURT
	45	529.4	37.7	700	4	BG547577	BG547577 602575404

#### ALIGNMENTS

##### RESULT 1

BQ712430

LOCUS BQ712430 995 bp mRNA linear EST 16-JUL-2002  
 DEFINITION AGENCOURT\_8352203 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6277729  
 5', mRNA sequence.  
 ACCESSION BQ712430  
 VERSION BQ712430.1 GI:21851329  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 995)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)



Qy 401 TTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAAC TG C T G T G C C T G 460  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 427 TTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAAC TG C T G T G C C T G 486

Qy 461 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCAA 520  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 487 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCAA 546

Qy 521 TC GG GT AACT CCC AGG AG AGT GT CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 580  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 547 TC GG GT AACT CCC AGG AG AGT GT CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 606

Qy 581 AGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAACACAAAGTCTACGCCTGCGAA 640  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 607 AGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAACACAAAGTCTACGCCTGCGAA 666

Qy 641 GTCACCCATCAGGGCCTGAGCTTGCCGTACAAAGAGCTTC-AACAGGGGAGAGTGT TA 699  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 667 GTCACCCATCAGGGCCTGAGCTGCCGTACAAAGAGCTTCNAACAGGGGAGAGTGT TA 726

Qy 700 G 700  
|  
Db 727 G 727

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 15, 2005, 12:20:41 ; Search time 121 Seconds  
(without alignments)  
8981.791 Million cell updates/sec

Title: US-10-698-041-1  
Perfect score: 2494  
Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlh  
-  
Q=/cgn2\_1/USPTO\_spool/US10698041/runat\_14042005\_155500\_6534/app\_query.fasta\_1.15  
43  
-DB=A\_Geneseq\_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10698041 @CGN\_1\_1\_149 @runat\_14042005\_155500\_6534 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1802	72.3	628	6	ABJ38670	Abj38670 Fab expe
2	1802	72.3	638	6	ADA89103	Ada89103 Phage dis
3	1802	72.3	638	6	ADA90139	Ada90139 Anti-Abet
4	1802	72.3	638	6	ADA91410	Ada91410 Anti-Abet
5	1802	72.3	747	7	ADG74355	Adg74355 MSPRO lig
6	1768.5	70.9	490	3	AAY56637	Aay56637 hCAT1 bin
7	1733	69.5	484	6	ABR55341	Abr55341 Amino aci
8	1676	67.2	537	3	AAB03664	Aab03664 Anti-CD18
9	1675	67.2	698	2	AAW83493	Aaw83493 4D5 Fab m
10	1668.5	66.9	650	5	ABP61241	Abp61241 Phage-dis
11	1665.5	66.8	502	8	ADN97515	Adn97515 Artificia
12	1664.5	66.7	512	8	ADN97497	Adn97497 Artificia
13	1660	66.6	517	8	ADN97495	Adn97495 Artificia
14	1658	66.5	519	8	ADN97493	Adn97493 Artificia
15	1650	66.2	713	8	ADN97491	Adn97491 Artificia
16	1648	66.1	715	8	ADN97489	Adn97489 Artificia
17	1606.5	64.4	487	6	ABO27163	Abo27163 Humanised
18	1282.5	51.4	712	8	ADN97543	Adn97543 Artificia
19	1213.5	48.7	1031	5	ADI46109	Adi46109 Single st
20	1178	47.2	483	8	ADN97549	Adn97549 Artificia
21	1178	47.2	510	8	ADN97519	Adn97519 Artificia
22	1178	47.2	510	8	ADN97501	Adn97501 Artificia
23	1178	47.2	700	8	ADN97521	Adn97521 Artificia
24	1142	45.8	219	8	ADR16817	Adr16817 Human bre
25	1115.5	44.7	500	7	ADD13792	Add13792 Plasmid p
26	1104	44.3	523	3	AAY44994	Aay44994 HD70scFv-
27	1098	44.0	239	7	ADE28405	Ade28405 Human ant
28	1097	44.0	238	8	ADL93650	Adl93650 Human CD4
29	1097	44.0	239	7	ADE28465	Ade28465 Human ant
30	1095	43.9	238	8	ADL93653	Adl93653 Human CD4
31	1094	43.9	238	8	ADL93654	Adl93654 Human CD4
32	1093	43.8	239	7	ADE28421	Ade28421 Human ant
33	1093	43.8	239	7	ADE28521	Ade28521 Human ant
34	1092	43.8	239	7	ADE28397	Ade28397 Human ant
35	1090	43.7	239	7	ADE28469	Ade28469 Human ant
36	1090	43.7	239	7	ADE28477	Ade28477 Human ant
37	1088	43.6	219	7	ADJ32150	Adj32150 Human int
38	1088	43.6	238	8	ADL93649	Adl93649 Human CD4
39	1082	43.4	238	8	ADL93652	Adl93652 Human CD4
40	1079	43.3	239	7	ADE28461	Ade28461 Human ant
41	1077.5	43.2	237	8	ADL93657	Adl93657 Human CD4
42	1077	43.2	239	3	AAY82615	Aay82615 Human PTH
43	1075.5	43.1	237	8	ADL93658	Adl93658 Human CD4
44	1075.5	43.1	237	8	ADL93651	Adl93651 Human CD4
45	1073	43.0	239	3	AAY82616	Aay82616 Human PTH

#### ALIGNMENTS

RESULT 1

ABJ38670

ID ABJ38670 standard; protein; 628 AA.

XX

AC ABJ38670;

XX

DT 26-JUN-2003 (first entry)

XX

DE Fab expression vector protein SEQ ID No 96.

XX

KW Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme;  
KW antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;  
KW constitutive activation; craniosynostosis; cell proliferative disorder;  
KW achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;  
KW hypochondroplasia; severe achondroplasia; transitional cell carcinoma;  
KW Muenke coronal craniosynostosis; Crouzin syndrome; acanthosis nigricans;  
KW tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma;  
KW mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein;  
KW Fab.

XX

OS Homo sapiens.

XX

PN WO2002102854-A2.

XX

PD 27-DEC-2002.

XX

PF 20-JUN-2002; 2002WO-IB003523.

XX

PR 20-JUN-2001; 2001US-0299187P.

XX

PA (MORP-) MORPHOSYS AG.

PA (PROC-) PROCHON BIOTECH LTD.

XX

PI Thomassen-Wolf E, Borges E, Yayon A, Rom E;

XX

DR WPI; 2003-167489/16.

XX

PT New molecules having the antigen-binding portion of antibodies that block  
PT activation of receptor protein tyrosine kinase, useful for treating or  
PT inhibiting skeletal dysplasias, craniosynostosis or cell proliferative  
PT disorders.

XX

PS Disclosure; Fig 26B; 103pp; English.

XX

CC The invention relates to a novel molecule comprising the antigen binding  
CC portion of an isolated antibody, which has an increased affinity for a  
CC receptor protein tyrosine kinase and which blocks constitutive activation  
CC of the receptor protein tyrosine kinase. The methods and compositions of  
CC the invention are useful for treating or inhibiting a skeletal dysplasia,  
CC craniosynostosis or a cell proliferative disorder. The skeletal dysplasia  
CC is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe  
CC achondroplasia with developmental delay or acanthosis nigricans  
CC dysplasia. The craniosynostosis disorder is Muenke coronal  
CC craniosynostosis or Crouzin syndrome with acanthosis nigricans. The cell  
CC proliferative disorder is tumour progression that is progression of  
CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple  
CC myeloma or mammary carcinoma. This sequence represents the protein

CC derived from a Fab expression vector relating to the protein tyrosine  
CC kinase inhibitor of the invention  
XX  
SQ Sequence 628 AA;

Alignment Scores:

Pred. No.:	1.3e-132	Length:	628
Score:	1802.00	Matches:	370
Percent Similarity:	83.47%	Conservative:	24
Best Local Similarity:	78.39%	Mismatches:	52
Query Match:	72.25%	Indels:	26
DB:	6	Gaps:	7

US-10-698-041-1 (1-1405) x ABJ38670 (1-628)

Qy	8	CTGGCTGGTTCGCTACCGTGGCCCAGGCAGGCGAGCTCGTGATGACTCAGTCTCCACTC	67
Db	2	LeuAlaGlyPheAlaThrValAlaGln---AlaAspIleValLeuThrGlnSerProAla	20
Qy	68	TCCCTGCCCGTCACCCCTGGAGAGGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTC	127
Db	21	ThrLeuSerLeuSerProGlyGluArgAlaThrLeuSerCysArgAlaSerGlnSerVal	40
Qy	128	CTGCATAGTAATGGATAACAATATTGGATTGGTACCTGCAGAACGCCAGGGCAGTCTCCA	187
Db	41	SerSerSer-----TyrLeuAlaTrpTyrGlnGlnLysProGlyGlnAlaPro	56
Qy	188	CAGCTCCTGATCTATTGGGTTTAATCGGGCCTCCGGGTCCCTGACAGGTTCACTGGC	247
Db	57	ArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyValProAlaArgPheSerGly	76
Qy	248	AGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGC	307
Db	77	SerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGluProGluAspPheAla	96
Qy	308	GTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTCGGCCAAGGGACACGACTG	367
Db	97	ValTyrTyrCysGlnGlnHisTyrThrProThrPheGlyGlnGlyThrLysVal	116
Qy	368	GAGATTAAACGAACGTGGCTGCACCCTCTGTCTTCATCTTCCGCCATCTGATGAGCAG	427
Db	117	GluIleLysArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGln	136
Qy	428	TTGAAATCTGGAACCTGCCTCTGTTGTGCTGCTGAATAACTCTATCCCAGAGAGGCC	487
Db	137	LeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAla	156
Qy	488	AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACA	547
Db	157	LysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThr	176
Qy	548	GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA	607
Db	177	GluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAla	196
Qy	608	GACTACGAGAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGC	667

Qy	197	AspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerPro	216
Db	668	GTCACAAAGAGCTCAACAGGGGAGAGTGTAGTTCTAGATAATTAAATTAGGAGGAATT	727
Db	217	ValThrLysSerPheAsnArgGlyGluAla-----	226
Qy	728	AAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCAACCA	787
Db	227	---MetLysGln-----SerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrPro	243
Qy	788	---GCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTCAGCCTGGGGGG	844
Db	244	ValThrLysAlaGlnValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGly	263
Qy	845	TCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCACTGG	904
Db	264	SerLeuArgLeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrp	283
Qy	905	GTCCGCCAACCTCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGGGAGT	964
Db	284	ValArgGlnAlaProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGly	303
Qy	965	ATCACAAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGCCAAG	1024
Db	304	SerThrTyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLys	323
Qy	1025	AACACGCTGTATCTGGAAATGAACAGTCTGAGAGGCCGAGGACACGGCTGTCTATTACTGT	1084
Db	324	AsnThrLeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCys	343
Qy	1085	ACACGAGATATTGGGGGTCGTGATGCT-----CACTGGGCCAGGGAAC	1129
Db	344	AlaArg-----TrpGlyGlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThr	361
Qy	1130	CTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCC	1189
Db	362	LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer	381
Qy	1190	TCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCCTGGTCAAGGACTACTTCCCC	1249
Db	382	SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro	401
Qy	1250	GAACCGGTGACGGTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCG	1309
Db	402	GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro	421
Qy	1310	GCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC	1369
Db	422	AlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSer	441
Qy	1370	AGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT	1405
Db	442	SerLeuGlyThrGlnThrTyrIleCysAsnValAsn	453

us-10-698-041-1.n2p.rapb

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 15, 2005, 14:34:27 ; Search time 165 Seconds  
(without alignments)  
5660.373 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 2494

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 2843670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=x1h  
-Q=/cgn2\_1/USPTO\_spool/US10698041/runat\_14042005\_155503\_6665/app\_query.fasta\_1.1543  
-DB=Published\_Applications\_AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10698041@CGN\_1\_1\_128@runat\_14042005\_155503\_6665  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

us-10-698-041-1.n2p.rapb  
 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	1699.5	68.1	4852	15	US-10-412-406-33	Sequence 33, Appl
2	1697.5	68.1	663	15	US-10-412-406-32	Sequence 32, Appl
3	1668.5	66.9	491	13	US-10-011-125-2	Sequence 2, Appl
4	1665.5	66.8	502	16	US-10-679-620-88	Sequence 88, Appl
5	1664.5	66.7	512	16	US-10-679-620-70	Sequence 70, Appl
6	1660	66.6	517	16	US-10-679-620-68	Sequence 68, Appl
7	1658	66.5	519	16	US-10-679-620-66	Sequence 66, Appl
8	1650	66.2	713	16	US-10-679-620-64	Sequence 64, Appl
9	1648	66.1	715	16	US-10-679-620-62	Sequence 62, Appl
10	1282.5	51.4	712	16	US-10-679-620-116	Sequence 116, Appl
11	1178	47.2	483	16	US-10-679-620-122	Sequence 122, Appl
12	1178	47.2	510	16	US-10-679-620-74	Sequence 74, Appl
13	1178	47.2	510	16	US-10-679-620-92	Sequence 92, Appl
14	1178	47.2	700	16	US-10-679-620-94	Sequence 94, Appl
15	1142	45.8	219	16	US-10-698-041-4	Sequence 4, Appl
16	1098	44.0	239	15	US-10-292-088-16	Sequence 16, Appl
17	1097	44.0	238	16	US-10-663-244-145	Sequence 145, Appl
18	1097	44.0	239	15	US-10-292-088-56	Sequence 56, Appl
19	1095	43.9	238	16	US-10-663-244-148	Sequence 148, Appl
20	1094	43.9	238	16	US-10-663-244-149	Sequence 149, Appl
21	1093	43.8	239	15	US-10-292-088-32	Sequence 32, Appl
22	1093	43.8	239	15	US-10-292-088-102	Sequence 102, Appl
23	1092	43.8	239	15	US-10-292-088-8	Sequence 8, Appl
24	1090	43.7	239	15	US-10-292-088-64	Sequence 64, Appl
25	1090	43.7	239	15	US-10-292-088-80	Sequence 80, Appl
26	1088	43.6	219	10	US-09-972-656-104	Sequence 104, Appl
27	1088	43.6	238	16	US-10-663-244-144	Sequence 144, Appl
28	1082	43.4	238	16	US-10-663-244-147	Sequence 147, Appl
29	1079	43.3	239	15	US-10-292-088-40	Sequence 40, Appl
30	1077.5	43.2	237	16	US-10-663-244-152	Sequence 152, Appl
31	1075.5	43.1	237	16	US-10-663-244-146	Sequence 146, Appl
32	1075.5	43.1	237	16	US-10-663-244-153	Sequence 153, Appl
33	1067	42.8	239	15	US-10-108-260A-4028	Sequence 4028, Appl
34	1060	42.5	239	10	US-09-992-600A-8	Sequence 8, Appl
35	1060	42.5	239	10	US-09-924-340-8	Sequence 8, Appl
36	1060	42.5	239	10	US-09-992-095B-8	Sequence 8, Appl
37	1060	42.5	239	10	US-09-999-570-8	Sequence 8, Appl
38	1060	42.5	239	14	US-10-000-489-8	Sequence 8, Appl
39	1060	42.5	239	14	US-10-000-986-8	Sequence 8, Appl
40	1060	42.5	239	14	US-10-154-678-8	Sequence 8, Appl
41	1060	42.5	239	17	US-10-838-854-8	Sequence 8, Appl
42	1052.5	42.2	220	9	US-09-822-698A-24	Sequence 24, Appl
43	1048	42.0	247	15	US-10-466-164-69	Sequence 69, Appl
44	1047	42.0	219	10	US-09-972-656-106	Sequence 106, Appl
45	1044	41.9	239	15	US-10-404-724-12	Sequence 12, Appl

#### RESULT 15

US-10-698-041-4

; Sequence 4, Application US/10698041  
 ; Publication No. US20040151724A1

GENERAL INFORMATION:  
 APPLICANT: Coronella-Wood, Julia  
 TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer  
 FILE REFERENCE: 5051.057  
 CURRENT APPLICATION NUMBER: US/10/698,041  
 CURRENT FILING DATE: 2003-10-30  
 PRIOR APPLICATION NUMBER: US 60/423,052  
 PRIOR FILING DATE: 2002-10-31  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 4  
 LENGTH: 219  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-698-041-4

## Alignment Scores:

Pred. No.:	6.37e-69	Length:	219
Score:	1142.00	Matches:	219
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.79%	Indels:	0
DB:	16	Gaps:	0

US-10-698-041-1 (1-1405) x US-10-698-041-4 (1-219)

Qy	41 GAGCTCGTGATGACTCAGTCCTCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCC	100
Db	1 GluLeuValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer	20
Qy	101 ATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACATTGGATTGG	160
Db	21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp	40
Qy	161 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGTTTAATCGGGCC	220
Db	41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlyPheAsnArgAla	60
Qy	221 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTATAACACTGAAAATC	280
Db	61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspTyrThrLeuLysIle	80
Qy	281 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCT	340
Db	81 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGlyLeuGlnThrPro	100
Qy	341 AGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACCTGGCTGCACCATCTGTC	400
Db	101 ArgThrPheGlyGlnGlyThrArgLeuGluIleLysArgThrValAlaAlaProSerVal	120
Qy	401 TTCACTTCCC GCCATCTGATGAGCAGTTGAAATCTGGAAC TG CCTCTGTTGTGCCTG	460
Db	121 PheIlePheProProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeu	140
Qy	461 CTGAATAACTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCAA	520
Db	141 LeuAsnAsnPheTyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGln	160
Qy	521 TCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC	580
Db	161 SerGlyAsnSerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu	180
Qy	581 AGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAACACAAAGTCTACGCCCTCGAA	640

us-10-698-041-1.n2p.rapb

Db 181 SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGlu 200

Qy 641 GTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 697

Db 201 ValThrHisGlnGlyLeuSerLeuProValThrLysSerPheAsnArgGlyGluCys 219

Search completed: April 15, 2005, 14:54:48

Job time : 190 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 15, 2005, 14:02:16 ; Search time 31.5 Seconds  
(without alignments)  
8583.146 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 2494

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlh

-

Q=/cgn2\_1/USPTO\_spool/US10698041/runat\_14042005\_155501\_6556/app\_query.fasta\_1.15  
43  
-DB=PIR\_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10698041@CGN\_1\_1\_37@runat\_14042005\_155501\_6556 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	897	36.0	215	2	JE0242	Ig kappa chain NIG
2	874	35.0	215	2	JE0244	Ig kappa chain NIG
3	856	34.3	215	2	JE0243	Ig kappa chain NIG
4	848.5	34.0	216	2	JE0241	Ig kappa chain Am3
5	843	33.8	215	2	A23746	Ig kappa chain V-I
6	800	32.1	219	2	S52028	Ig kappa chain - m
7	800	32.1	219	2	PC4203	Ig kappa chain (mo
8	789	31.6	219	2	S16112	Ig kappa chain V r
9	785	31.5	219	2	S38865	Ig kappa chain - m
10	778	31.2	217	2	S42772	Ig kappa chain - m
11	756	30.3	225	2	JL0029	Ig kappa chain pre
12	741.5	29.7	240	2	S06084	Ig kappa chain pre
13	728	29.2	220	2	A49444	Ig gamma-1 heavy c
14	702.5	28.2	220	2	A31790	Ig kappa chain V r
15	693.5	27.8	218	2	S68241	Ig kappa chain V r
16	680.5	27.3	218	2	JC5810	monoclonal antibod
17	677.5	27.2	214	2	S68212	Ig kappa chain (Ma
18	665	26.7	548	2	S38864	Ig epsilon chain C
19	660.5	26.5	241	2	S69131	Ig heavy chain (DO
20	655.5	26.3	210	2	A56169	Ig kappa chain V r
21	655.5	26.3	213	2	S68213	Ig heavy chain (Ma
22	655.5	26.3	234	2	S01320	Ig kappa chain pre
23	655	26.3	197	2	S29593	Ig kappa chain (WM
24	649.5	26.0	230	2	S33161	Ig kappa chain - s
25	646.5	25.9	234	2	S14237	Ig kappa chain pre
26	639.5	25.6	225	2	S37484	Ig kappa chain - m
27	633	25.4	178	2	PT0219	Ig kappa chain V-C
28	627	25.1	235	2	S25058	Ig kappa chain - m
29	626	25.1	444	2	PC4436	monoclonal antibod
30	621	24.9	220	2	S68211	Ig heavy chain (Ma
31	600.5	24.1	254	2	B31790	Ig heavy chain V r
32	598.5	24.0	246	2	S38950	Ig gamma chain - m
33	598.5	24.0	446	2	S40295	Ig gamma-2a chain
34	594	23.8	135	2	S40342	Ig kappa chain - h
35	594	23.8	135	2	S52059	JC-kappa protein -
36	593.5	23.8	469	2	S37483	Ig gamma-2a chain
37	593	23.8	121	2	S40371	Ig kappa chain - h
38	592	23.7	474	1	G2MS11	Ig gamma-2b chain
39	576	23.1	214	2	PC4202	monoclonal antibod
40	571	22.9	136	2	S40357	Ig kappa chain V-J
41	570.5	22.9	221	2	S49220	Ig gamma-1 chain -
42	565	22.7	470	2	S22080	Ig heavy chain pre
43	560	22.5	117	1	K2HUGM	Ig kappa chain pre
44	559	22.4	143	2	S23624	Ig heavy chain V r
45	557	22.3	132	2	S26882	Ig kappa chain V r

us-10-698-041-1.n2p.rup

GenCore version 5.1.6  
copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 15, 2005, 12:25:16 ; Search time 145.5 Seconds  
(without alignments)  
9889.639 Million cell updates/sec

Title: US-10-698-041-1  
Perfect score: 2494  
Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=x1h  
-Q=/cgn2\_1/USPTO\_spool/US10698041/runat\_14042005\_155501\_6542/app\_query.fasta\_1.1543  
-DB=UniProt\_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10698041@CGN\_1\_1\_197@runat\_14042005\_155501\_6542 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1097	44.0	239	2	Q8NEK0	Q8nek0 homo sapien
2	1070.5	42.9	240	2	Q6PIH6	Q6pih6 homo sapien
3	992	39.8	239	2	Q8TCDO	Q8tcd0 homo sapien
4	992	39.8	239	2	Q6P491	Q6p491 homo sapien
5	904.5	36.3	236	2	Q6PIL8	Q6pil8 homo sapien
6	888	35.6	235	2	Q6GMV9	Q6gmv9 homo sapien

## us-10-698-041-1.n2p.rup

7	888	35.6	470	2	Q6PJA4	Q6pja4 homo sapien
8	878	35.2	235	2	Q6PJF2	Q6pjf2 homo sapien
9	877.5	35.2	236	2	Q6P5S8	Q6p5s8 homo sapien
10	876	35.1	478	2	Q6PI81	Q6pi81 homo sapien
11	873.5	35.0	466	2	Q6N096	Q6n096 homo sapien
12	865	34.7	235	2	Q6GMW0	Q6gmw0 homo sapien
13	864.5	34.7	472	2	Q6N089	Q6n089 homo sapien
14	852.5	34.2	236	2	Q6GMW1	Q6gmw1 homo sapien
15	852	34.2	465	2	Q6P6C4	Q6p6c4 homo sapien
16	849.5	34.1	234	2	Q7Z473	Q7z473 homo sapien
17	846.5	33.9	236	2	Q6GMX0	Q6gmx0 homo sapien
18	845	33.9	466	2	Q6IN78	Q6in78 homo sapien
19	842.5	33.8	473	2	Q6MZV7	Q6mzv7 homo sapien
20	838.5	33.6	236	2	Q6GMX8	Q6gmx8 homo sapien
21	838.5	33.6	236	2	Q7Z3Y4	Q7z3y4 homo sapien
22	836	33.5	544	2	Q6PJ95	Q6pj95 homo sapien
23	835.5	33.5	236	2	Q6PIT5	Q6pit5 homo sapien
24	835	33.5	236	2	Q6ZP85	Q6zp85 homo sapien
25	834	33.4	475	2	Q6MZQ6	Q6mzq6 homo sapien
26	833.5	33.4	236	2	Q6PIH7	Q6pih7 homo sapien
27	829.5	33.3	464	2	Q6MZU6	Q6mzu6 homo sapien
28	827	33.2	470	2	Q7Z5W1	Q7z5w1 homo sapien
29	818.5	32.8	236	2	Q6GMX9	Q6gmx9 homo sapien
30	815.5	32.7	475	2	Q6GMW7	Q6gmw7 homo sapien
31	812	32.6	473	2	Q6P055	Q6p055 homo sapien
32	808.5	32.4	236	2	Q6PIH4	Q6pih4 homo sapien
33	807	32.4	480	2	Q6N094	Q6n094 homo sapien
34	792.5	31.8	521	2	Q8N4Y9	Q8n4y9 homo sapien
35	789	31.6	219	2	Q65ZC0	Q65zc0 mus musculu
36	785.5	31.5	482	2	Q7Z351	Q7z351 homo sapien
37	772	31.0	475	2	Q6N095	Q6n095 homo sapien
38	765	30.7	481	2	Q6N097	Q6n097 homo sapien
39	761.5	30.5	465	2	Q6GMX6	Q6gmx6 homo sapien
40	759	30.4	493	2	Q68CN4	Q68cn4 homo sapien
41	741	29.7	476	2	Q6GMX1	Q6gmx1 homo sapien
42	736.5	29.5	518	2	Q6N030	Q6n030 homo sapien
43	734.5	29.5	469	2	Q7Z7P5	Q7z7p5 homo sapien
44	725	29.1	480	2	Q6PJF1	Q6pjf1 homo sapien
45	702	28.1	417	2	Q6N093	Q6n093 homo sapien

us-10-698-041-1.rni

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 08:20:56 ; Search time 263 Seconds  
(without alignments)  
8741.326 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 1405

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:/\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:/\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:/\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:/\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:/\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	958.4	68.2	5925	4	US-09-315-926A-78	Sequence 78, Appl
2	901.4	64.2	4691	3	US-08-591-632-43	Sequence 43, Appl
3	901.4	64.2	4691	3	US-09-611-451-43	Sequence 43, Appl
4	901.4	64.2	6166	3	US-08-591-632-51	Sequence 51, Appl
5	901.4	64.2	6166	3	US-09-611-451-51	Sequence 51, Appl
6	779.8	55.5	6563	3	US-09-027-449-61	Sequence 61, Appl
7	779.8	55.5	6563	3	US-08-804-444A-61	Sequence 61, Appl
8	779.8	55.5	6563	3	US-09-026-985-61	Sequence 61, Appl
9	779.8	55.5	6563	3	US-09-121-952A-61	Sequence 61, Appl
10	779.8	55.5	6563	3	US-09-234-340A-61	Sequence 61, Appl
11	747.4	53.2	2178	1	US-08-463-587A-24	Sequence 24, Appl
12	747.4	53.2	2178	2	US-08-463-667A-2	Sequence 2, Appl
13	747.4	53.2	2178	3	US-08-923-854-24	Sequence 24, Appl
14	747.4	53.2	2178	5	PCT-US91-09133-25	Sequence 25, Appl
15	739.6	52.6	1951	4	US-10-011-125A-1	Sequence 1, Appl
16	738.6	52.6	2143	3	US-09-097-309-5	Sequence 5, Appl
17	738.6	52.6	2143	3	US-09-097-171A-9	Sequence 9, Appl

					us-10-698-041-1.rni	
18	738.6	52.6	2143	3	US-09-460-587-5	Sequence 5, Appli
19	738.6	52.6	2143	4	US-09-940-166A-5	Sequence 5, Appli
20	738.6	52.6	6550	3	US-09-422-712B-1	Sequence 1, Appli
21	738.6	52.6	6550	3	US-09-607-756-1	Sequence 1, Appli
22	734.6	52.3	6127	2	US-08-887-352B-1	Sequence 1, Appli
23	734.6	52.3	6127	3	US-09-109-207C-1	Sequence 1, Appli
24	734.6	52.3	6127	3	US-09-296-005-1	Sequence 1, Appli
25	734.6	52.3	6127	4	US-09-920-171-1	Sequence 1, Appli
26	734.6	52.3	6127	4	US-09-716-028-1	Sequence 1, Appli
27	734.6	52.3	6127	4	US-10-113-996-1	Sequence 1, Appli
28	632.2	45.0	3169	3	US-08-630-820-5	Sequence 5, Appli
29	632.2	45.0	3169	4	US-09-273-453-5	Sequence 5, Appli
30	604.6	43.0	968	4	US-10-000-489-7	Sequence 7, Appli
31	566.4	40.3	1632	2	US-08-792-824-8	Sequence 8, Appli
32	566.4	40.3	1644	2	US-08-792-824-11	Sequence 11, Appli
33	564.8	40.2	1672	2	US-08-792-824-2	Sequence 2, Appli
34	564.8	40.2	4435	2	US-08-792-824-1	Sequence 1, Appli
35	542.8	38.6	720	3	US-08-487-550-5	Sequence 5, Appli
36	542.8	38.6	720	4	US-09-526-098-5	Sequence 5, Appli
37	542.8	38.6	720	4	US-09-383-916-5	Sequence 5, Appli
38	542.4	38.6	1641	2	US-08-792-824-5	Sequence 5, Appli
39	522.8	37.2	729	1	US-08-398-613A-55	Sequence 55, Appli
40	522.8	37.2	729	1	US-08-398-612A-55	Sequence 55, Appli
41	522.8	37.2	729	1	US-08-398-611A-55	Sequence 55, Appli
42	522.8	37.2	729	1	US-08-396-851A-55	Sequence 55, Appli
43	522.8	37.2	729	2	US-08-491-334A-55	Sequence 55, Appli
44	522.8	37.2	729	3	US-09-027-449-41	Sequence 41, Appli
45	522.8	37.2	729	3	US-08-804-444A-41	Sequence 41, Appli

## ALIGNMENTS

### RESULT 1

US-09-315-926A-78

; Sequence 78, Application US/09315926A

Patent No. 6498027

; GENERAL INFORMATION:

APPLICANT: Es van, Helmuth

APPLICANT: Havenga, Menzo

APPLICANT: Verlinden, Stefan

TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

FILE REFERENCE: 2183-4080US

CURRENT APPLICATION NUMBER: US/09/315,926A

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: EP 99201593.3

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: EP 98201693.3

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PatentIn version 3.0

SEQ ID NO 78

LENGTH: 5925

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: misc\_feature

OTHER INFORMATION: Description of Artificial Sequence: phage

NAME/KEY: primer\_bind

LOCATION: (1)..(5925)

OTHER INFORMATION: /note="Nucleotide hcAT1 encoding sequence

US-09-315-926A-78

us-10-698-041-1.rni

Query Match 68.2%; Score 958.4; DB 4; Length 5925;  
 Best Local Similarity 83.5%; Pred. No. 1.2e-257;  
 Matches 1147; Conservative 0; Mismatches 196; Indels 31; Gaps 4;

Qy	51	TGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGGCCGGCCTCCATCTCCTGCA	110
Db	2339	TCACGCAGTCTCCAGGCATCCTGTCTTGCTCCGGGGCAGGAGCCACCCCTCCTGCA	2398
Qy	111	GGTCTAGTCAGAGTCTCTGCATAGTAATGGATACAACATTGGATTGGTACCTGCAGA	170
Db	2399	GGGCCAGTCAGAGTGTCAAGCAGCAGAAC-----TTAGCCTGGTACCAGCAGA	2446
Qy	171	AGCCAGGGCAGTCTCACAGCTCCTGATCTATTGGTTTAATGGGCTCCGGGTCC	230
Db	2447	AACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGTATCAAACAGGGCACTGGCGTCC	2506
Qy	231	CTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGG	290
Db	2507	CAGACAGGTTCACTGGCAGTGGCTGGGCAAGACTCACTCTCACCATCACAGACTGG	2566
Qy	291	AGGCTGAGGATGTTGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTCG	350
Db	2567	AGCCTGAAGATTTGCGGTGTATTACTTCAGCGGTATGGCAGGTCACTGTGGACGTTG	2626
Qy	351	GCCAAGGGACACGACTGGAGATTAAAC---GAACCTGGCTGCACCCTGTCTTCATCT	407
Db	2627	GTCAAGGGACCAAGGTGGAGATCAAACGTGGAACCTGGCTGCACCATCTGTCTTCATCT	2686
Qy	408	TCCC GCCATCTGATGAGCAGTTGAAACTGGAACTGCCTCTGTTGTGCGCTGCTGAATA	467
Db	2687	TCCC GCCATCTGATGAGCAGTTGAAACTGGAACTGCCTCTGTTGTGCGCTGCTGAATA	2746
Qy	468	ACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCAATCGGGTA	527
Db	2747	ACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCAATCGGGTA	2806
Qy	528	ACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	587
Db	2807	ACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	2866
Qy	588	CCCTGACGCTGAGCAAAGCAGACTACGGAGAAACACAAAGTCAAGCCTGCGAAGTCACCC	647
Db	2867	CCCTGACGCTGAGCAAAGCAGACTACGGAGAAACACAAAGTCAAGCCTGCGAAGTCACCC	2926
Qy	648	ATCAGGGCTGAGCTTGCCTCACAAAGAGCTTCAACAGGGGAGAGTGTAA-----G	700
Db	2927	ATCAGGGCTGAGTTACCGGTGACAAAGAGCTTCAACAGGGGAGAGTGTAAATAAGGCG	2986
Qy	701	TTCTAGATAATTAAATTAGGAGGAATTAAAATGAAATACCTATTGCCTACGGCAGCCGCT	760
Db	2987	CGCCAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCT	3046
Qy	761	GGATTGTTATTACTCGCTGCCCAACCAGCCATGCCAGGTGCAGCTGCAGGAGTCCGGG	820
Db	3047	GGATTGTTATTACTCGCGGCCAGCCGCCATGCCAGGTCCAGCTGGTGCAGTCTGGG	3106
Qy	821	GGAGGCTTAGTTCAGCCTGGGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACC	880
Db	3107	GGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCA	3166
Qy	881	TTCAGCAATTACTGGATGCACTGGTCCGCCACCTCCAGGGAAGGGCTGGTGTGGTC	940
Db	3167	TTCAGTAGCTATGCTATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTG	3226

us-10-698-041-1.rni

Qy	941	TCACGTATTAATGAAGATGGGAGTATCACAAACGACGCCGGACTCCGTGAAGGGCCGATCC	1000
Db	3227	GCAGTTATATCATATGATGGAAGCAATAAATACGAGACTCCGTGAAGGGCCGATT	3286
Qy	1001	ACCATCTCCAGAGACAACGCCAACGCTGTATCTGGAAATGAACAGTCTGAGAGCC	1060
Db	3287	ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCT	3346
Qy	1061	GAGGACACGGCTGTCTATTACTGTACACGAGATATTGGGG-----GTCGTGATGCT	1111
Db	3347	GAGGACACGGCTGTGTATTACTGTGCGAGAGGGATTACAGTAACTAAATCACGATTGAC	3406
Qy	1112	CACTGGGCCAGGGAACCCCTGGTACCGTCTCCTCAGCCTCCACCAAGGGCCATCGTC	1171
Db	3407	TACTGGGCCAGGGCACCCCTGGTACCGTCTCAAGCGCCTCCACCAAGGGCCATCGTC	3466
Qy	1172	TTCCCCCTGGCACCCCTCCAAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCCTG	1231
Db	3467	TTCCCCCTGGCACCCCTCCAAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCCTG	3526
Qy	1232	GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTTGAACTCAGGCGCCCTGACCAGC	1291
Db	3527	GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTTGAACTCAGGCGCCCTGACCAGC	3586
Qy	1292	GGCGTGCACACCTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG	1351
Db	3587	GGCGTCCACACCTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTA	3646
Qy	1352	GTGACCGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTGAAT	1405
Db	3647	GTGACCGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTGAAT	3700

us-10-698-041-1.n2p.rai

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 15, 2005, 14:10:36 ; Search time 27.5 Seconds  
(without alignments)  
7627.777 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 2494

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=x1h  
-Q=/cgn2\_1/usPTO\_spool/US10698041/runat\_14042005\_155502\_6573/app\_query.fasta\_1.1543  
-DB=Issued\_Patents\_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10698041@CGN\_1\_1\_30@runat\_14042005\_155502\_6573 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_AA:  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1668.5	66.9	491	4	US-10-011-125A-2	Sequence 2, Appli
2	1060	42.5	239	4	US-10-000-489-8	Sequence 8, Appli

us-10-698-041-1.n2p.ra1

3	1005.5	40.3	239	3	US-08-487-550-6	Sequence 6, Appli
4	1005.5	40.3	239	4	US-09-526-098-6	Sequence 6, Appli
5	1005.5	40.3	239	4	US-09-383-916-6	Sequence 6, Appli
6	982.5	39.4	248	4	US-09-315-926A-80	Sequence 80, Appli
7	979	39.3	238	4	US-09-698-705-10	Sequence 10, Appli
8	960	38.5	242	1	US-08-398-613A-56	Sequence 56, Appli
9	960	38.5	242	1	US-08-398-612A-56	Sequence 56, Appli
10	960	38.5	242	1	US-08-398-611A-56	Sequence 56, Appli
11	960	38.5	242	2	US-08-491-334A-56	Sequence 56, Appli
12	960	38.5	242	3	US-09-027-449-42	Sequence 42, Appli
13	960	38.5	242	3	US-08-804-444A-42	Sequence 42, Appli
14	960	38.5	242	3	US-09-026-985-42	Sequence 42, Appli
15	960	38.5	242	4	US-09-121-952A-42	Sequence 42, Appli
16	960	38.5	242	4	US-09-234-340A-42	Sequence 42, Appli
17	951.5	38.2	218	4	US-09-698-705-12	Sequence 12, Appli
18	927	37.2	599	1	US-08-442-542-18	Sequence 18, Appli
19	927	37.2	599	3	US-08-765-469-18	Sequence 18, Appli
20	915.5	36.7	240	4	US-09-301-593-36	Sequence 36, Appli
21	907	36.4	241	2	US-07-916-098A-56	Sequence 56, Appli
22	904	36.2	242	3	US-09-027-449-51	Sequence 51, Appli
23	904	36.2	242	3	US-09-027-449-56	Sequence 56, Appli
24	904	36.2	242	3	US-09-027-449-62	Sequence 62, Appli
25	904	36.2	242	3	US-08-804-444A-51	Sequence 51, Appli
26	904	36.2	242	3	US-08-804-444A-56	Sequence 56, Appli
27	904	36.2	242	3	US-09-026-985-51	Sequence 51, Appli
28	904	36.2	242	3	US-09-026-985-56	Sequence 56, Appli
29	904	36.2	242	3	US-09-026-985-62	Sequence 62, Appli
30	904	36.2	242	4	US-09-121-952A-51	Sequence 51, Appli
31	904	36.2	242	4	US-09-121-952A-56	Sequence 56, Appli
32	904	36.2	242	4	US-09-121-952A-62	Sequence 62, Appli
33	904	36.2	242	4	US-09-234-340A-51	Sequence 51, Appli
34	904	36.2	242	4	US-09-234-340A-56	Sequence 56, Appli
35	904	36.2	242	4	US-09-234-340A-62	Sequence 62, Appli
36	902.5	36.2	220	3	US-08-952-235-1	Sequence 1, Appli
37	902.5	36.2	220	4	US-09-669-971-1	Sequence 1, Appli
38	902	36.2	239	4	US-09-627-896B-22	Sequence 22, Appli
39	900.5	36.1	226	4	US-09-456-090A-86	Sequence 86, Appli
40	900.5	36.1	226	4	US-09-453-234-86	Sequence 86, Appli
41	900	36.1	219	3	US-09-027-449-72	Sequence 72, Appli
42	900	36.1	219	3	US-09-026-985-72	Sequence 72, Appli
43	900	36.1	219	4	US-09-121-952A-72	Sequence 72, Appli
44	900	36.1	219	4	US-09-234-340A-72	Sequence 72, Appli
45	900	36.1	235	4	US-09-472-087-14	Sequence 14, Appli

## ALIGNMENTS

### RESULT 1

US-10-011-125A-2

Sequence 2, Application US/10011125A

Patent No. 6828121

#### GENERAL INFORMATION:

APPLICANT: Chen, Christina Yu-Ching

TITLE OF INVENTION: BACTERIAL HOST STRAINS

FILE REFERENCE: P1804R1

CURRENT APPLICATION NUMBER: US/10/011,125A

CURRENT FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 60/256,162

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 2

LENGTH: 491

TYPE: PRT

us-10-698-041-1.n2p.ra1

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
; Patent No. 6828121  
US-10-011-125A-2

### Alignment Scores:

Pred. No.: 1.23e-133 Length: 491  
Score: 1668.50 Matches: 340  
Percent similarity: 78.94% Conservative: 31  
Best Local Similarity: 72.34% Mismatches: 62  
Query Match: 66.90% Indels: 37  
DB: 4 Gaps: 7

US-10-698-041-1 (1-1405) x US-10-011-125A-2 (1-491)

us-10-698-041-1.n2p.ra1

Qy	758	GCTGGATTGTTATTACTCGCT---GCCCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAG	814
	:::: :::: :::	:::	
Db	247	AlaSerMetPheValPheSerIleAlaThrAsnAlaTyrAlaGluValGlnLeuValGlu	266
Qy	815	TCCGGGGGAGGCTTAGTTCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGA	874
Db	267	SerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAlaAlaSerGly	286
Qy	875	TACACCTTCAGCAATTACTGGATGCACTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTG	934
	::::             ::::		
Db	287	TyrThrPheThrAsnTyrGlyMetAsnTrpIleArgGlnAlaProGlyLysGlyLeuGlu	306
Qy	935	TGGGTCTCACGTATTAATGAA---GATGGGAGTATCACAAACGACGCCGGACTCCGTGAAG	991
Db	307	TrpValGlyTrpIleAsnThrTyrThrGlyGluProThrTyrAlaAlaAsp---PheLys	325
Qy	992	GGCCGATCCACCATCTCCAGAGACAACGCCAACGCTGTATCTGGAAATGAACAGT	1051
	::::       ::::		
Db	326	ArgArgPheThrIleSerAlaAspThrSerSerAsnThrValTyrLeuGlnMetAsnSer	345
Qy	1052	CTGAGAGCCGAGGACACGGCTGTCTATTACTGTACACGA-----	1090
	::::		
Db	346	LeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysTyrProHisTyrTyrGlySer	365
Qy	1091	-----GATATTGGGGTCGTGATGCTCACTGGGCCAGGGAACCCCTGGTC	1135
	::::		
Db	366	SerHisTrpTyrPheAspVal-----TrpGlyGlnGlyThrLeuVal	379
Qy	1136	ACCGTCTCCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCCCAAG	1195
Db	380	ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys	399
Qy	1196	AGCACCTCTGGGGCACAGCGGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG	1255
Db	400	SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro	419
Qy	1256	GTCGCGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTC	1315
Db	420	ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal	439
Qy	1316	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTG	1375
Db	440	LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerLeu	459
Qy	1376	GGCACCCAGACCTACATCTGCAACGTGAAT	1405
Db	460	GlyThrGlnThrTyrIleCysAsnValAsn	469

us-10-698-041-1.rng

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:39:44 ; Search time 814 Seconds  
(without alignments)  
10217.735 Million cell updates/sec

Title: US-10-698-041-1

Perfect score: 1405

Sequence: 1 aaaatgcctggctggttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1405	100.0	1405	13	ADR16814	Adr16814 Human bre
2	1014.8	72.2	1522	8	ACC00496	Acc00496 Humanised
3	1003	71.4	1514	12	ADG64751	Adg64751 Humanised
4	985.8	70.2	1424	13	ADR16815	Adr16815 Human bre
5	958.4	68.2	5924	3	AAZ38921	Aaz38921 hCAT1 bin
6	958.4	68.2	5925	3	AAZ38770	Aaz38770 hCAT1 clo
7	937.8	66.7	2186	10	ADD26469	Add26469 Phagemid
8	937.8	66.7	2790	10	ADD26467	Add26467 Phagemid
9	937.8	66.7	2810	10	ADD26471	Add26471 Phagemid
10	936.4	66.6	1440	10	ADD26475	Add26475 Phagemid

us-10-698-041-1.rng							
11	923	65.7	1539	8	AAD56202	Aad56202	X5 antibo
12	916.6	65.2	1539	8	AAD56203	Aad56203	X5 antibo
13	906.2	64.5	1680	12	ADF83552	Adf83552	Anti-tete
14	901.4	64.2	4691	2	AAQ92546	Aaq92546	pComb3 ex
15	901.4	64.2	6166	2	AAQ92547	Aaq92547	Expressio
16	884.8	63.0	10251	10	ABZ37478	Abz37478	CJRA05 nu
17	856	60.9	1526	12	ADN97514	Adn97514	Artificia
18	851.8	60.6	1551	12	ADN97496	Adn97496	Artificia
19	834.8	59.4	1566	12	ADN97494	Adn97494	Artificia
20	834	59.4	2154	12	ADN97490	Adn97490	Artificia
21	820.8	58.4	1572	12	ADN97492	Adn97492	Artificia
22	820	58.4	2160	12	ADN97488	Adn97488	Artificia
23	796.8	56.7	5679	13	ADP79576	Adp79576	Plasmid p
24	779.8	55.5	6563	2	AAV44953	Aav44953	Anti-IL-8
25	779.8	55.5	6563	2	AAX90579	Aax90579	p6G4V11N3
26	779.8	55.5	6563	3	AAZ87970	Aaz87970	Nucleotid
27	779.8	55.5	6563	3	AAC65509	Aac65509	Anti-IL-8
28	779.8	55.5	6563	8	ABX63890	Abx63890	Expressio
29	779.8	55.5	6563	8	ABX81417	Abx81417	Vector p6
30	779.8	55.5	6563	10	AAD59311	Aad59311	p6G4V11 N
31	767.8	54.6	6400	3	AAA53389	Aaa53389	Expressio
32	751.8	53.5	2000	9	ACC70052	Acc70052	Nucleotid
33	747.4	53.2	2178	2	AAQ25592	Aaq25592	Encodes 4
34	747.4	53.2	2178	2	AAV81689	Aav81689	4D5 Fab m
35	739.6	52.6	6072	2	AAV63493	Aav63493	Fab-displ
36	739.6	52.6	6072	6	ABN85200	Abn85200	Phage-dis
37	738.6	52.6	2143	2	AAX03840	Aax03840	Plasmid p
38	738.6	52.6	2143	5	AAF31463	Aaf31463	ps 1130 e
39	737.4	52.5	2050	13	ADR47463	Adr47463	pTTOD(gH3)
40	735.2	52.3	6072	2	AAV71266	Aav71266	VEGF huma
41	734.6	52.3	6127	2	AAX07474	Aax07474	Mus muscu
42	734.6	52.3	6127	4	AAF69253	Aaf69253	Expressio
43	734.6	52.3	6127	12	ADN07022	Adn07022	F(ab)-pha
44	733.2	52.2	1951	6	ABQ73919	Abq73919	Plasmid p
45	732.8	52.2	1477	12	ADQ07674	Adq07674	Nucleotid

## RESULT 2

ACC00496

ID ACC00496 standard; DNA; 1522 BP.

XX

AC ACC00496;

XX

DT 10-JUL-2003 (first entry)

XX

DE Humanised F3 Fab insert coding sequence.

XX

KW Cytostatic; Platelet-Derived Growth Factor; PDGF; antibody; tumour;  
KW cancer; F3 antibody; gene; ds.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 29. .682

FT /\*tag= a

FT /product= "FAB protein #1"

FT /transl\_except= (pos:98. .100,aa:Xaa)

FT /transl\_except= (pos:110. .112,aa:Xaa)

FT /transl\_except= (pos:119. .121,aa:Xaa)

FT /transl\_except= (pos:155. .157,aa:Xaa)

FT /transl\_except= (pos:215. .217,aa:Xaa)

FT /transl\_except= (pos:239. .241,aa:Xaa)